



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Rhode, Peter R.
Acevedo, Jorge
Burkhardt, Martin
Jiao, Jin-an
Wong, Hing C.
- (ii) TITLE OF THE INVENTION: SOLUBLE MHC COMPLEXES AND
METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 - (B) STREET: 130 Water Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: usa
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/766,378
 - (B) FILING DATE: 19-JAN-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/960,190
 - (B) FILING DATE: 29-OCT-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Corless, Peter F
 - (B) REGISTRATION NUMBER: 33,860
 - (C) REFERENCE/DOCKET NUMBER: 48002-DIV
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-523-3400
 - (B) TELEFAX: 617-523-6440
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCACCATG

8

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCCAAGC TTCCGGGCCA CCATGGCTCT GCAGATCCCC AGC

43

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCCACTT AAGGTCCTTG GGCTGCTCAG CACC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGGGGCCA TGGCCGAAA CTCCGAAAGG CATTTTCG

37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCGACTA GTCCACTCCA CAGTGATGGG GC

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGACTAG TCCAGTGTTT CAGAACCGGC TC

32

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGGGGATA TCTCTCAGGC TGTTCACGCT G

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGGGTTTCG AAAAGTGTAC TTACGGGGGG CTGGAATCTC AGTTTC

46

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGGGCTCG AGTATCAAAG AAGAACATGT GATCATC

37

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGCGGGAT CCGTTCTCTG TAGTCTCTGG GAGAGG

36

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATAAGAGGA AGAAGAGTAC ATGCCGATGG AACCCGGGTG AG

42

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTCTTCAC CCGGGTTCCA TCGGCATGTA CTCTTCTTCC TCG

43

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCCGCTA GCGGAGGGGG CGGAAGCGGC GGAGGGGGGG ACACCCGACC ACGTTTCCTG 60
TGGCAGCCTA AGAGG 75

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCCGAAT TCCCCACTAG TCCATTCCAC TGTGAGAGGG CTTGTCAC 48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGGGGCCA TGGCCTACGA CAGAACCCCG TGGTG 35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGACTA GTTCGCCGCT GCACTGTGAA GC 32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGGGGTATG·CATACGACGA GAACCCCGTG GTG

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGGGGACTA GTCCACTTCG AGGAACTGTT TCC

33

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCCTGGTC TCCTCTGTGA GTGG

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTCTCACAG AGGAGACCAG GAGG

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCCACC G TTACGACAA GCCCGTGGTG 30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCCATCG ATAAGTG TAC TTACGTGGGA GAGGGCTTGG AGCAT 45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 6...1505
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG	50
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val	
1 5 10 15	
GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT	98
Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala	
20 25 30	
GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA	146
Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly	
35 40 45	
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC	194
Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val Val	
50 55 60	

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile Arg 65 70 75	242
CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp 80 85 90 95	290
AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp 100 105 110	338
GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala 115 120 125	386
GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC Glu Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser 130 135 140	434
ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser 145 150 155	482
AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr 160 165 170 175	530
GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln 180 185 190	578
GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp 195 200 205	626
TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly 210 215 220	674
GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile 225 230 235	722
ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC Thr Val Glu Trp Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 240 245 250 255	770
GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Asp Asp Ile 260 265 270	818
GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro 275 280 285	866

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC	914
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe	
290 295 300	
TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT	962
Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe	
305 310 315	
GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT	1010
Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala	
320 325 330 335	
GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC	1058
Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr	
340 345 350	
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT	1106
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro	
355 360 365	
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC	1154
Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile	
370 375 380	
TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC	1202
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val	
385 390 395	
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC	1250
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser	
400 405 410 415	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT	1298
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile	
420 425 430	
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA	1346
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys	
435 440 445	
CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT	1394
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr	
450 455 460	
GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG	1442
Val Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val	
465 470 475	
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA	1490
Gly Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg	
480 485 490 495	
CAC CCA GGG CCT TTA TGA	1508
His Pro Gly Pro Leu	
500	

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Ala	Leu	Gln	Ile	Pro	Ser	Leu	Leu	Leu	Ser	Ala	Ala	Val	Val	Val
1				5				10					15		
Leu	Met	Val	Leu	Ser	Ser	Pro	Arg	Thr	Leu	Ser	Ile	Ser	Gln	Ala	Val
			20					25					30		
His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly	Arg	Ala	Ser	Gly	Gly
		35					40					45			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Ser	Glu	Arg	His	Phe	Val	Val	Gln
	50					55				60					
Phe	Lys	Gly	Glu	Cys	Tyr	Tyr	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu
65					70				75					80	
Val	Thr	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Val	Arg	Tyr	Asp	Ser
			85					90					95		
Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	Pro	Asp	Ala
		100						105					110		
Glu	Tyr	Trp	Asn	Ser	Gln	Pro	Glu	Ile	Leu	Glu	Arg	Thr	Arg	Ala	Glu
	115					120					125				
Val	Asp	Thr	Ala	Cys	Arg	His	Asn	Tyr	Glu	Gly	Pro	Glu	Thr	Ser	Thr
	130					135				140					
Ser	Leu	Arg	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser	Leu	Ser	Arg
145				150					155					160	
Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp
		165						170					175		
Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu
	180						185					190			
Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp
	195					200					205				
Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His	Gln	Gly	Glu
	210					215				220					
Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr
225			230						235					240	
Val	Glu	Trp	Thr	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly
		245						250					255		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Glu	Asp	Asp	Ile	Glu
	260					265						270			
Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly
	275					280				285					
Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr
	290				295					300					
Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly
305				310					315					320	
Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala
		325					330					335			
Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro
		340					345					350			

Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro	Val
		355					360					365			
Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe
		370					375					380			
Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr
		385				390				395					400
Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser	Phe
				405					410					415	
His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr
			420					425						430	
Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	His
		435					440					445			
Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Val
		450					455					460			
Val	Cys	Ala	Leu	Gly	Leu	Ser	Val	Gly	Leu	Val	Gly	Ile	Val	Val	Gly
		465				470				475					480
Thr	Ile	Phe	Ile	Ile	Gln	Gly	Leu	Arg	Ser	Gly	Gly	Thr	Ser	Arg	His
				485				490						495	
Pro	Gly	Pro	Leu												
			500												

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Ser	Gln	Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala	Pro	Tyr	Ser	Thr	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Glu	Thr	Pro
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
1 5 10 15
Arg Thr Pro Pro
20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Glu Glu Glu Glu Tyr Met Pro Met Glu Pro Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TSGGGGSGGG GSGGGSGGG GSSS

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg
1				5					10					15	
Thr	Pro	Pro													

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser	Ser	Ala	Asp	Leu	Val	Pro	Arg	Gly	Ser	Thr	Thr	Ala	Pro	Ser	Ala
1				5					10					15	
Gln	Leu	Glu	Lys	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Asn	Ala	Gln	Leu
			20					25						30	
Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	Leu	Ala	Gln			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser	Ser	Ala	Asp	Leu	Val	Pro	Arg	Gly	Ser	Thr	Thr	Ala	Pro	Arg	Ala
1				5					10					15	

Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu
 20 25 30
 Lys Trp Lys Leu Gln Ala Leu Lys Lys Leu Ala Gln
 35 40

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ASSGGGSGGG

10

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 1 5 10 15
 Ser Tyr Ile Tyr Ala
 20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His
 1 5 10 15
 Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr
 20 25 30
 Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg
 35 40 45
 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln
 50 55 60

Lys	Asp	Ile	Leu	Glu	Gln	Ala	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg
65					70					75					80
His	Asn	Tyr	Gly	Val	Val	Glu	Ser	Phe	Thr	Val	Gln	Arg	Arg		
				85					90						

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile	Lys	Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro
1				5				10					15		
Asp	Gln	Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe
			20					25					30		
His	Val	Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe
			35				40					45			
Gly	Arg	Phe	Ala	Ser	Phe	Glu	Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala
			50			55				60					
Val	Asp	Lys	Ala	Asn	Leu	Glu	Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Thr
65				70						75				80	
Pro	Ile	Thr	Asn	Val	Pro	Pro	Glu	Val	Thr	Val	Leu	Thr	Asn	Ser	Pro
				85				90					95		
Val	Glu	Leu	Arg	Glu	Pro	Asn	Val	Leu	Ile	Cys	Phe	Ile	Asp	Lys	Phe
			100					105					110		
Thr	Pro	Pro	Val	Val	Asn	Val	Thr	Trp	Leu	Arg	Asn	Gly	Lys	Pro	Val
			115				120					125			
Thr	Thr	Gly	Val	Ser	Glu	Thr	Val	Phe	Leu	Pro	Arg	Glu	Asp	His	Leu
			130				135				140				
Phe	Arg	Lys	Phe	His	Tyr	Leu	Pro	Phe	Leu	Pro	Ser	Thr	Glu	Asp	Val
145				150						155				160	
Tyr	Asp	Cys	Arg	Val	Glu	His	Trp	Gly	Leu	Asp	Glu	Pro	Leu	Leu	Lys
				165					170				175		
His	Trp	Glu	Phe	Asp	Ala	Pro	Ser	Pro	Leu	Pro	Glu	Thr	Thr	Glu	Asn
			180					185					190		